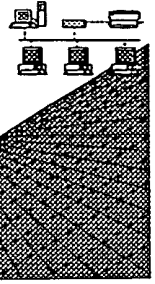


McElwain

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/049,304
Art Unit / Team No. : 1649
Date Processed by STIC: 1/31/2000

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

on Elwain

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304

DATE: 02/02/2000
TIME: 22:09:34

INPUT SET: S34610.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

1
2
3 (1) General Information:
4
5 (i) APPLICANT: EPELBAUM, SABINE URSULA
6 FALCO, SAVERIO CARL
7 MCDEVITT, RAYMOND ERVIN, III
8
9 (ii) TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR
10 INCREASING THE LYSINE CONTENT OF
11 THE SEEDS OF PLANTS
12
13 (iii) NUMBER OF SEQUENCES: 132
14
15 (iv) CORRESPONDENCE ADDRESS:
16 (A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
17 (B) STREET: 1007 MARKET STREET
18 (C) CITY: WILMINGTON
19 (D) STATE: DELAWARE
20 (E) COUNTRY: U.S.A.
21 (F) ZIP: 19898
22
23 (v) COMPUTER READABLE FORM:
24 (A) MEDIUM TYPE: DISKETTE, 3.50 INCH
25 (B) COMPUTER: IBM PC COMPATIBLE
26 (C) OPERATING SYSTEM: MICROSOFT OFFICE 97
27 (D) SOFTWARE: MICROSOFT WINDOWS 95
28
29 (vi) CURRENT APPLICATION DATA:
30 (A) APPLICATION NUMBER:
31 (B) FILING DATE:
32 (C) CLASSIFICATION:
33
34 (vii) PRIOR APPLICATION DATA:
35 (A) APPLICATION NUMBER: 08/824,627
36 (B) FILING DATE: MARCH 27, 1997
37
38 (viii) ATTORNEY/AGENT INFORMATION:
39 (A) NAME: CHRISTENBURY, LYNNE M.
40 (B) REGISTRATION NUMBER: 30,971
41 (C) REFERENCE/DOCKET NUMBER: BB-1037-F
42
43 (ix) TELECOMMUNICATION INFORMATION:
44 (A) TELEPHONE: 302-992-5481
45 (B) TELEFAX: 302-892-7949

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304

DATE: 02/02/2000
 TIME: 22:09:35

INPUT SET: S34610.raw

46 (C) TELEX: 835420
 47
 48

ERRORED SEQUENCES FOLLOW:

237 (2) INFORMATION FOR SEQ ID NO:6:
 238
 239 (i) SEQUENCE CHARACTERISTICS: *(see p. 3)*
 240 (A) LENGTH: 917 base pairs
 241 (B) TYPE: nucleic acid
 242 (C) STRANDEDNESS: single
 243 (D) TOPOLOGY: linear
 244
 245 (ii) MOLECULE TYPE: DNA (genomic)
 246
 247 (ix) FEATURE:
 248 (A) NAME/KEY: CDS
 249 (B) LOCATION: 3..911
 250
 251 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
 252
 253 CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC 47
 254 Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
 255 1 5 10 15
 256
 257 ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC 95
 258 Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile
 259 20 25 30
 260
 261 GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC 143
 262 Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly
 263 35 40 45
 264
 265 TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA 191
 266 Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr
 267 50 55 60
 268
 269 ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT 239
 270 Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val
 271 65 70 75
 272
 273 GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG 287
 274 Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg
 275 80 85 90 95
 276
 277 ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC 335
 278 Thr Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly
 279 100 105 110
 280

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304

DATE: 02/02/2000
TIME: 22:09:35

INPUT SET: S34610.raw

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281 CTT TTA GTT GTA ACT CCT TAT TAC TCC AAG CCG AGC CAA GAG GGA TTG 383
282 Leu Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu
283           115                      120                      125
284
285 CTG GCG CAC TTC GGT GCA ATT GCT GCA GCA ACA GAG GTT CCA ATT TGT 431
286 Leu Ala His Phe Gly Ala Ile Ala Ala Thr Glu Val Pro Ile Cys
287           130                      135                      140
288
289 CTC TAT GAC ATT CCT GGT CGG TCA GGT ATT CCA ATT GAG TCT GAT ACC 479
290 Leu Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr
291           145                      150                      155
292
293 ATG AGA CGC CTG AGT GAA TTA CCT ACG ATT TTG GCG GTC AAG GAC GCC 527
294 Met Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala
295 160                      165                      170                      175
296
297 AAG GGT GAC CTC GTT GCA GCC ACG TCA TTG ATC AAA GAA ACG GGA CTT 575
298 Lys Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu
299           180                      185                      190
300
301 GCC TGG TAT TCA GGC GAT GAC CCA CTA AAC CTT GTT TGG CTT GCT TTG 623
302 Ala Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu
303           195                      200                      205
304
305 GGC GGA TCA GGT TTC ATT TCC GTA ATT GGA CAT GCA GCC CCC ACA GCA 671
306 Gly Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala
307           210                      215                      220
308
309 TTA CGT GAG TTG TAC ACA AGC TTC GAG GAA GGC GAC CTC GTC CGT GCG 719
310 Leu Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala
311           225                      230                      235
312
313 CGG GAA ATC AAC GCC AAA CTA TCA CCG CTG GTA GCT GCC CAA GGT CGC 767
314 Arg Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg
315 240                      245                      250                      255
316
317 TTG GGT GGA GTC AGC TTG GCA AAA GCT GCT CTG CGT CTG CAG GGC ATC 815
318 Leu Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
319           260                      265                      270
320
321 AAC GTA GGA GAT CCT CGA CTT CCA ATT ATG GCT CCA AAT GAG CAG GAA 863
322 Asn Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu
323           275                      280                      285
324
--> 325 CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GCT GGA GTT CTA TAA TGAGAATTC 918
326 Leu Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu *
327           290                      295                      300
328

```

918
917

1982 (2) INFORMATION FOR SEQ ID NO:76:
1983
1984 (i) SEQUENCE CHARACTERISTICS:
1985 (A) LENGTH: 175 base pairs

(next page)

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304

DATE: 02/02/2000
TIME: 22:09:35

INPUT SET: S34610.raw

1986 (B) TYPE: nucleic acid
 1987 (C) STRANDEDNESS: double
 1988 (D) TOPOLOGY: linear
 1989
 1990 (ii) MOLECULE TYPE: DNA (genomic)
 1991
 1992 (vi) ORIGINAL SOURCE:
 1993 (B) STRAIN: E. coli
 1994 (G) CELL TYPE: DH5 alpha
 1995
 1996 (vii) IMMEDIATE SOURCE:
 1997 (B) CLONE: 5-1
 1998
 1999 (ix) FEATURE:
 2000 (A) NAME/KEY: CDS
 2001 (B) LOCATION: 2..172
 2002 (D) OTHER INFORMATION: /function= "synthetic
 2003 storage protein
 2004 /product= "protein"
 2005 /gene= "ssp"
 2006 /standard_name=
 2007 "5.5.5.7.7.7.7.5"

2009 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

2010
 2011 C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46
 2012 Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
 2013 1 5 10 15
 2014
 2015 GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG 94
 2016 Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
 2017 20 25 30
 2018
 2019 AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG 142
 2020 Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
 2021 35 40 45
 2022
 --> 2023 AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG
 2024 Lys Ala Met Glu Glu Lys Met Lys Ala
 2025 50 55
 2026

179/195

3026 (2) INFORMATION FOR SEQ ID NO:111:

3027
 3028 (i) SEQUENCE CHARACTERISTICS:
 --> 3029 (A) LENGTH: 3194 base pairs 3195 slow (p.7)
 3030 (B) TYPE: nucleic acid
 3031 (C) STRANDEDNESS: double
 3032 (D) TOPOLOGY: linear
 3033
 3034 (ii) MOLECULE TYPE: DNA (genomic)
 3035
 3036 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304DATE: 02/02/2000
TIME: 22:09:36

INPUT SET: S34610.raw

3037
3038 ATGAATTCAA ATGGCCATGA GGAGGAGAAG AAGTTGGGGA ATGGAGTTGT GGGGATTCTA 60
3039
3040 TCTGAAACAG TTAACAAATG GGAGAGACGA ACACCATTGA CGCCATCGCA TTGCGCTCGC 120
3041
3042 CTTTTACACG GTGGGAAAGA CAGAACCGGC ATTTCCCGCA TTGTGGTTCA GCCATCTGCT 180
3043
3044 AAGCGTATCC ATCATGATGC CTTGTATGAA CATGTTGGGT GTGAAATTTT TGATGATTTG 240
3045
3046 TCTGATTGTG GGCTTATACT TGAATCAA CAACCTGAGC TAGAAATGAT TCTTCCAGAG 300
3047
3048 AGAGCATACG CTTTCTTTTC ACATACTCAT AAGGCACAGA AAGAGAACAT GCCTTTGTTG 360
3049
3050 GATAAAATTC TTTCTGAGAG AGTGACTTTG TGTGATTATG AGCTCATTGT TGGGGATCAT 420
3051
3052 GGGAAACGAT TATTGGCGTT TGGTAAATAT GCAGGCAGAG CTGGTCTTGT TGACTTCTTA 480
3053
3054 CACGGACTTG GACAGCGATA TCTAAGTCTA GGATACTCAA CACCTTTCCT CTCGCTCGGT 540
3055
3056 GCATCGTATA TGTATTCCTC ATTGGCTGCT GCAAAAGCCG CTGTAATTTT TGTGTTGTA 600
3057
3058 GAAATTGCAA GCCAGGGACT GCCATTAGGA ATCTGCCCTC TTGTATTTGT CTTACCCGGA 660
3059
3060 ACAGGAAATG TTTCTCTGGG GCGCAAGAA ATTTTCAAGC TTCTTCCTCA CACTTTTGTT 720
3061
3062 GAACCAAGCA AACTTCCTGA ACTATTTGTA AAA

Agarose blank section

09/049304

GACAAAG GAATTAGTCA AAATGGGATT 780

3063
3064 TCAACAAAGC GAGTCTATCA AGTATATGGT TGTATTATTA CCAGCCAAGA CATGGTTGAA 840
3065
3066 CACAAAGATC CATCAAAGTC ATTCGACAAA GCCGACTATT ATGCACACCC GGAACATTAC 900
3067
3068 AATCCAGTTT TCCACGAAAA GATATCGCCA TATACGTCTG TTCTTGTAAG CTGTATGTAC 960
3069
3070 TGGGAGAAGA GGTTCCTG TCTTCTGAGC ACAAACAGC TTCAAGATT AACAAAAAA 1020
3071
3072 GGACTCCAC TAGTAGGCAT ATGTGATATA ACTTGTGACA TCGGTGGCTC CATTGAATTT 1080
3073
3074 GTTAACCGAG CTACTTTAAT CGATTCCCCT TTCTTCAGGT TTAATCCCTC GAACAATTCA 1140
3075
3076 TACTACGATG ACATGGATGG GGATGGCGTA CTATGCATGG CTGTTGACAT TTTACCCACA 1200
3077
3078 GAATTTGCAA AAGAGGCATC CCAGCATTTT GGAGATATTC TTTCCGGATT TGTCGGTAGT 1260
3079
3080 TTGGCTTCAA TGACTGAAAT TTCAGATCTA CCAGCACATC TGAAGAGGGC TTGCATAAGC 1320
3081
3082 TATAGGGGAG AATTGACATC TTTGTATGAG TATATTCCAC GTATGAGGAA GTCAAATCCA 1380
3083
3084 GAAGAGGCAC AAGATAATAT TATCGCCAAC GGGGTTTCCA GCCAGAGAAC ATTCAACATA 1440
3085
3086 TTGGTATCTC TGAGCGGACA CCTATTTGAT AAGTTTCTGA TAAACGAAGC TCTTGATATG 1500
3087
3088 ATCGAAGCGG CTGGTGGCTC ATTTCAATTG GCTAAATGTG AACTGGGGCA GAGCGCTGAT 1560
3089

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304DATE: 02/02/2000
TIME: 22:09:36

INPUT SET: S34610.raw

3090	GCTGAATCGT	ACTCAGAACT	TGAAGTTGGT	GCGGATGATA	AGAGAGTATT	GGATCAAATC	1620
3091							
3092	ATTGATTCAT	TAACTCGGTT	AGCTAATCCA	AATGAAGATT	ATATATCCCC	ACATAGAGAA	1680
3093							
3094	GCAAATAAGA	TCTCACTGAA	GATTGGTAAA	GTCCAGCAAG	AAAATGAGAT	AAAAGAGAAG	1740
3095							
3096	CCTGAAATGA	CGAAAAAATC	AGGTGTTTTG	ATTCTTGGTG	CTGGACGTGT	GTGTGCGCCA	1800
3097							
3098	GCTGCTGATT	TCCTAGCTTC	AGTTAGAACC	ATTTCGTAC	AGCAATGGTA	CAAAACATAT	1860
3099							
3100	TTCGGAGCAG	ACTCTGAAGA	GAAAACAGAT	GTCATGTGA	TTGTGCGGTC	TCTGTATCTT	1920
3101							
3102	AAGGATGCCA	AAGAGACGGT	TGAAGGTATT	TCAGATGTAG	AAGCAGTTCG	GCTAGATGTA	1980
3103							
3104	TCTGATAGTG	AAAGTCTCCT	TAAGTATGTT	TCTCAGGTTG	ATGTTGTCCT	AAGTTTATTA	2040
3105							
3106	CCTGCAAGTT	GTCATGCTGT	TGTAGCAAAG	ACATGCATTG	AGCTGAAGAA	GCATCTCGTC	2100
3107							
3108	ACTGCTAGCT	ATGTTGATGA	TGAAACGTCC	ATGTTACATG	AGAAGGCTAA	GAGTGCTGGG	2160
3109							
3110	ATAACGATTC	TAGGCGAAAT	GGGACTGGAC	CCTGGAATCG	ATCACATGAT	GGCGATGAAA	2220
3111							
3112	ATGATCAACG	ATGCTCATAT	CAAAAAAGGG	AAAGTGAAGT	CTTTTACCTC	TTATTGTGGA	2280
3113							
3114	GGGCTTCCCT	CTCCTGCTGC	AGCAAATAAT	CCATTAGCAT	ATAAATTTAG	CTGGAACCCCT	2340
3115							
3116	GCTGGAGCAA	TTCGAGCTGG	TCAAAACCCC	GCCAAATACA	AAAGCAACGG	CGACATAATA	2400
3117							
3118	CATGTTGATG	GGAAGAATCT	CTATGATTCC	GCGGCAAGAT	TCCGAGTACC	TAATCTTCCA	2460
3119							
3120	GCTTTTGCAT	TGGAGTGTTT	TCCAAATCGT	GA CTCCTTGG	TTTACGGGGA	ACATTATGGC	2520
3121							
3122	ATCGAGAGCG	AAGCAACAAC	GATATTTTCGT	GGAACACTCA	GATATGAAGG	GTTTAGTATG	2580
3123							
3124	ATAATGGCAA	CACTTTTCGAA	ACTTGGATTG	TTTGACAGTG	AAGCAAATCA	AGTACTCTCC	2640
3125							
3126	ACTGAAAAGA	GGATTACGTT	TGGTGCTCTT	TTAAGTAACA	TTCTAAATAA	GGATGCAGAC	2700
3127							
3128	AATGAATCAG	AGCCCCTAGC	GGGAGAAGAA	GAGATAAGCA	AGAGAATTAT	CAAGCTTGGA	2760
3129							
3130	CATTCCAAGG	AGACTGCAGC	CAAAGCTGCC	AAAACAATTG	TATTCTTGGG	GTTCAACGAA	2820
3131							
3132	GAGAGGGAGG	TTCCATCACT	GTGTAAGAGC	GTATTTGATG	CAACTTGTTA	CCTAATGGAA	2880
3133							
3134	GAGAACTAG	CTTATTCCGG	AAATGAACAG	GACATGGTGC	TTTTCATCA	CGAAGTAGAA	2940
3135							
3136	GTGGAATTCC	TTGAAAGCAA	ACGTATAGAG	AAGCACACTG	CGACTCTTTT	GGAATTCGGG	3000
3137							
3138	GACATCAAGA	ATGGACAAAC	AACAACCGCT	ATGGCCAAGA	CTGTTGGGAT	CCCTGCAGCC	3060
3139							
3140	ATTGGAGCTC	TGGTGTTAAT	TGAAGACAAG	ATCAAGACAA	GAGGAGTCTT	AAGGCCTCTC	3120
3141							
3142	GAAGCAGAGG	TGTATTTGCC	AGCTTTGGAT	ATATTGCAAG	CATATGGTAT	AAAGCTGATG	3180

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/049,304

DATE: 02/02/2000
TIME: 22:09:37

INPUT SET: S34610.raw

3143
3144 GAGAAGGCAG AATGA
3145

3195

3359 (2) INFORMATION FOR SEQ ID NO:113:

3360

3361 (i) SEQUENCE CHARACTERISTICS:

--> 3362 (A) LENGTH: 23 base pairs

3363 (B) TYPE: nucleic acid

3364 (C) STRANDEDNESS: single

3365 (D) TOPOLOGY: linear

3366

3367 (ii) MOLECULE TYPE: DNA (genomic)

3368

3369 (xi) SEQUENCE DESCRIPTION: 'SEQ ID NO:113:

3370

--> 3371 TTYT(C)CAYA (C)CAYAARGC (C)CA

3372

23

I is invalid for use in the sequence - use N and explain in

*(ix) FEATURE:
section*

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/049,304DATE: 02/02/2000
TIME: 22:09:37*INPUT SET: S34610.raw*

Line	Error	Original Text
325	# of Sequences for line conflicts w/ running total	CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GC
2023	# of Sequences for line conflicts w/ running total	AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATA
3029	Entered (3194) and Calc. Seq. Length (3195) differ	(A)LENGTH: 3194 base pairs
3362	Entered (23) and Calc. Seq. Length (20) differ	(A)LENGTH: 23 base pairs
3371	Wrong Nucleic Acid Designator	TTYTCICAYA CICA YAARGC ICA
3371	Wrong Nucleic Acid Designator	TTYTCICAYA CICA YAARGC ICA
3371	Wrong Nucleic Acid Designator	TTYTCICAYA CICA YAARGC ICA
3371	# of Sequences for line conflicts w/ running total	TTYTCICAYA CICA YAARGC ICA